

Machine learning applications for Radiomics

Citation for published version (APA):

Parmar, C. (2017). *Machine learning applications for Radiomics: towards robust non-invasive predictors in clinical oncology*. [Doctoral Thesis, Maastricht University]. Datawyse / Universitaire Pers Maastricht. <https://doi.org/10.26481/dis.20170518cmp>

Document status and date:

Published: 01/01/2017

DOI:

[10.26481/dis.20170518cmp](https://doi.org/10.26481/dis.20170518cmp)

Document Version:

Publisher's PDF, also known as Version of record

Please check the document version of this publication:

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Summary

In order to enhance the applications of radiomics, in this thesis, we conducted different radiomic analyses on large patient cohorts of non-small cell lung cancer and head and neck cancer.

Part-1 Assessing variability in radiomics:

In the first part, the focus was on assessing publicly available semi-automatic segmentation tools. These tools were evaluated in terms of their efficiency and reproducibility and were compared to the manual segmentations. Also, reproducibility of radiomic features with respect to different segmentation methods were also assessed. **Chapter-2 & 3** presented the studies where publicly available semiautomatic segmentation methods were assessed for their clinical relevance. Overall, it was observed that semiautomatic segmentation methods tend to provide faster and more reproducible segmentations as compared to manual delineations. Moreover, in **Chapter-4**, It was observed that radiomic features extracted from the volumes, which are delineated by semiautomatic segmentation methods, had significantly higher reproducibility as compared to the features extracted from the manually segmented volumes. These results indicated that semiautomatic segmentation methods could provide a better alternative to the manual delineation for radiomic analyses.

Part-2 Machine learning methods for radiomics

In this part, different unsupervised and supervised machine learning methods were investigated for radiomics based prognostic/predictive analyses. These different methods of feature selection/reduction and prediction modeling were compared in terms of their performance and robustness. **Chapter-5** presented a radiomic analysis of 1,019 patients with lung or head-and-neck cancer. It was found that radiomic signature have prognostic power in independent data sets of lung and head-and-neck cancer patients. Moreover, the radiogenomic analysis of this study revealed that a prognostic radiomic signature, capturing intratumor heterogeneity, was also associated with underlying gene-expression patterns. These independent cohorts were further investigated in **Chapter-6** for their cancer specific grouping and prognostic characteristics. This analysis indicated both common as well as cancer-specific clustering and clinical associations of

radiomic features. In an exploratory study presented in **Chapter-7**, the association between radiomic features and the tumor histologic subtypes (adenocarcinoma and squamous cell carcinoma) were investigated in the cohorts of non-small cell lung cancer patients. Histological subtypes can influence the choice of a treatment/therapy for lung cancer patients. We observed that radiomic features show significant association with the lung tumor histology.

Highly accurate and reliable machine-learning approaches can drive the success of radiomic applications in clinical care. In **Chapter-8 & 9**, different machine-learning methods were examined in terms of their performance and stability for predicting overall survival in independent lung and head & neck cancer cohorts. To ensure the unbiased evaluation of different machine-learning methods, publicly available implementations along with reported parameter configurations were used. The variability analysis indicated that the choice of classification method was the most dominant source of performance variation. Identification of optimal machine-learning methods for radiomic applications is a crucial step towards stable and clinically relevant radiomic biomarkers, providing a non-invasive way of quantifying and monitoring tumor-phenotypic characteristics in clinical practice.

At the end, **Chapter 10** provided a general discussion of the results presented in this thesis and related future perspectives.